

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2002, 06:41:09 ; Search time 1759.97 Seconds
(without alignments)
187.471 Million cell updates/sec

Title: US-08-887-505-117

Perfect score: 20
Sequence: 1 TTNGCGACCCCACTACTC 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

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11: gb_sts:*

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20: em_or:*

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25: em_ro:*

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27: em_sy:*

28: em_un:*

29: em_vi:*

30: em_htgo_hum:*

31: em_htgo_inv:*

32: em_htgo_rod:*

33: em_htg_hum:*

34: em_htg_inv:*

35: em_htg_rod:*

36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	19	95.0	27	6	AR106359	AR106359 Sequence
C 2	19	95.0	33	6	AR004396	AR004396 Sequence
C 3	19	95.0	33	6	AR064935	AR064935 Sequence
C 4	19	95.0	33	6	AR097188	AR097188 Sequence
C 5	19	95.0	33	6	AR130866	AR130866 Sequence
C 6	19	95.0	33	6	IB2871	IB2871 Sequence 50
C 7	19	95.0	40	6	ARI53179	ARI53179 Sequence
C 8	19	95.0	46	6	IA4581	IA4581 Sequence 10
C 9	19	95.0	46	6	I70986	I70986 Sequence 10
C 10	19	95.0	139	14	AF282631	AF282631 Hepatitis
C 11	19	95.0	139	14	AF282632	AF282632 Hepatitis
C 12	19	95.0	139	14	AF282633	AF282633 Hepatitis
C 13	19	95.0	139	14	AF282634	AF282634 Hepatitis
C 14	19	95.0	139	14	AF282635	AF282635 Hepatitis
C 15	19	95.0	139	14	AF282637	AF282637 Hepatitis
C 16	19	95.0	139	14	AF282638	AF282638 Hepatitis
C 17	19	95.0	139	14	AF282639	AF282639 Hepatitis
C 18	19	95.0	139	14	AF282640	AF282640 Hepatitis
C 19	19	95.0	139	14	AF282641	AF282641 Hepatitis
C 20	19	95.0	139	14	AF282642	AF282642 Hepatitis
C 21	19	95.0	139	14	AF282643	AF282643 Hepatitis
C 22	19	95.0	139	14	AF282644	AF282644 Hepatitis
C 23	19	95.0	139	14	AF282645	AF282645 Hepatitis
C 24	19	95.0	139	14	AF282646	AF282646 Hepatitis
C 25	19	95.0	139	14	AY003921	AY003921 Hepatitis
C 26	19	95.0	139	14	AY003922	AY003922 Hepatitis
C 27	19	95.0	139	14	AY003923	AY003923 Hepatitis
C 28	19	95.0	139	14	AY003924	AY003924 Hepatitis
C 29	19	95.0	139	14	AY003925	AY003925 Hepatitis
C 30	19	95.0	139	14	AY003928	AY003928 Hepatitis
C 31	19	95.0	139	14	AY003929	AY003929 Hepatitis
C 32	19	95.0	139	14	AY003930	AY003930 Hepatitis
C 33	19	95.0	139	14	AY003932	AY003932 Hepatitis
C 34	19	95.0	139	14	AY003933	AY003933 Hepatitis
C 35	19	95.0	139	14	AY003934	AY003934 Hepatitis
C 36	19	95.0	139	14	AY003935	AY003935 Hepatitis
C 37	19	95.0	139	14	AY003936	AY003936 Hepatitis
C 38	19	95.0	139	14	AY003937	AY003937 Hepatitis
C 39	19	95.0	139	14	AY003938	AY003938 Hepatitis
C 40	19	95.0	139	14	AY003939	AY003939 Hepatitis
C 41	19	95.0	139	14	AY003940	AY003940 Hepatitis
C 42	19	95.0	139	14	AY003941	AY003941 Hepatitis
C 43	19	95.0	139	14	AY003942	AY003942 Hepatitis
C 44	19	95.0	139	14	AY003943	AY003943 Hepatitis
C 45	19	95.0	139	14	AY003944	AY003944 Hepatitis

ALIGNMENTS

RESULT 1
LOCUS AR106359/c 27 bp DNA
DEFINITION Sequence 21 from patent US 6107028.
ACCESSION AR106359
VERSION AR106359.1 GI:12820889
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kay, M.A. and Lieber, A.
TITLE Ribozymes for treating hepatitis C
JOURNAL Patent: US 6107028-A 21 22-AUG-2000;
FEATURES
source Location/Qualifiers
1..27
/organism="unknown"
BASE COUNT 6 a 4 c 12 g 5 t
ORIGIN

14-FEB-2001

PAT

Fri Jan 11 09:31:11 2002

us-08-887-505-117.rge

Page 2

Query Match
Best Local Similarity 95.0%; Score 19; DB 6; Length 27;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTTCGGACCCCAACTACTC 20
Db 24 TTTCGGACCCCAACTACTC 5

RESULT 2
LOCUS AR004396
DEFINITION Sequence 33 bp DNA
ACCESSION AR004396 PAT 04-DEC-1998
VERSION AR004396.1 GI:3965275
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan, P., Chang, C., Running, J. and Urdea, M.S.
TITLE Nucleic acid probes immobilized on polystyrene surfaces
JOURNAL Patent: US 5747244-A 50 05-MAY-1998;
FEATURES Location/Qualifiers
source
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match
Best Local Similarity 95.0%; Score 19; DB 6; Length 33;
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Db 10 TTTCGGACCCCAACTACTC 29

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DEFINITION Sequence 33 bp DNA
ACCESSION AR064935 PAT 29-SEP-1998
VERSION AR064935.1 GI:5995151
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Urdea, M.S., Horn, T., Chang, C., Warner, B. and Fu
TITLE Nucleic acid hybridization assays employing large
JOURNAL branched polynucleotides
FEATURES Patent: US 5849481-A 60 15-DEC-1998;
source Location/Qualifiers
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTTCGGACCCCAACTACTC 20
Db 10 TTTCGGACCCCAACTACTC 29

RESULT 4
LOCUS AR097188

LOCUS AR097188
DEFINITION Sequence 126 from patent US 6071693.
ACCESSION AR097188 PAT 14-FEB-2001
VERSION AR097188.1 GI:12805918
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6071693-A 126 06-JUN-2000;
FEATURES Location/Qualifiers
source
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match
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Db 10 TTTCGGACCCCAACTACTC 29

RESULT 5
LOCUS AR130686
DEFINITION Sequence 33 bp DNA
ACCESSION AR130686 PAT 16-MAY-2001
VERSION AR130686.1 GI:14119011
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6190864-A 126 20-FEB-2001;
FEATURES Location/Qualifiers
source
BASE COUNT 8 a 13 c 6 g 6 t
ORIGIN

Query Match
Best Local Similarity 95.0%; Score 19; DB 6; Length 33;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTTCGGACCCCAACTACTC 20
Db 10 TTTCGGACCCCAACTACTC 29

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LOCUS 182871
DEFINITION Sequence 50 from patent US 5712383.
ACCESSION 182871 PAT 10-JUN-1998
VERSION 182871.1 GI:3211168
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Sheridan, P., Chang, C., Running, J. and Urdea, M.S.
TITLE process for immobilizing nucleic acid probes on surfaces

Query Match 95.0%; Score 19; DB 6; Length 46;
Best Local Similarity 95.0%; Pred. No. 0.69;
Matches 19; Conservative 0; Mismatches 1; Indels

BASE COUNT	28 a	36 c	43 g	32 t
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Query Match          95.0%; Score 19; DB 14; Length 139;
Best Local Similarity 95.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTNGCGACCCCAACTACTC 20
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Db 116 TTGCGACCCCAACTACTC 97

RESULT 11
AF282632/c
LOCUS      AF282632      139 bp      RNA      VRL      01-MAR-2001
DEFINITION Hepatitis C virus isolate H069 clone II 5' non-coding region
sequence.
ACCESSION  AF282632
VERSION     AF282632.1 GI:10764495
KEYWORDS
SOURCE      Hepatitis C virus.
ORGANISM    Hepatitis C virus.
REFERENCE   1 (bases 1 to 139)
AUTHORS     Harris,K.A. and Teo,C.G.
TITLE       Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
JOURNAL     Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED     11139197
REFERENCE   2 (bases 1 to 139)
AUTHORS     Harris,K.A. and Teo,C.G.
TITLE       Direct Submission
JOURNAL     Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK

FEATURES             Location/Qualifiers
     source           1. .139
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                     /isolate="H069"
                     /db_xref="taxon:11103"
                     /clone="II"
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BASE COUNT      28 a      36 c      42 g      33 t
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Best Local Similarity 95.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTNGCGACCCCAACTACTC 20
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Db 116 TTGCGACCCCAACTACTC 97

RESULT 12
AF282633/c
LOCUS      AF282633      139 bp      RNA      VRL      01-MAR-2001
DEFINITION Hepatitis C virus isolate H071 clone I 5' non-coding region
sequence.
ACCESSION  AF282633
VERSION     AF282633.1 GI:10764496
KEYWORDS
SOURCE      Hepatitis C virus.
ORGANISM    Hepatitis C virus.
REFERENCE   1 (bases 1 to 139)
AUTHORS     Harris,K.A. and Teo,C.G.
TITLE       Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
JOURNAL     Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED     11139197
REFERENCE   2 (bases 1 to 139)
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Query Match          95.0%; Score 19; DB 14; Length 139;
Best Local Similarity 95.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTNGCGACCCCAACTACTC 20
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Db 116 TTGCGACCCCAACTACTC 97

RESULT 13
AF282634/c
LOCUS      AF282634      139 bp      RNA      VRL      01-MAR-2001
DEFINITION Hepatitis C virus isolate H071 clone II 5' non-coding region
sequence.
ACCESSION  AF282634
VERSION     AF282634.1 GI:10764497
KEYWORDS
SOURCE      Hepatitis C virus.
ORGANISM    Hepatitis C virus.
REFERENCE   1 (bases 1 to 139)
AUTHORS     Harris,K.A. and Teo,C.G.
TITLE       Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
JOURNAL     Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED     11139197
REFERENCE   2 (bases 1 to 139)
AUTHORS     Harris,K.A. and Teo,C.G.
TITLE       Direct Submission
JOURNAL     Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK

FEATURES             Location/Qualifiers
     source           1. .139
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Best Local Similarity 95.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 116 TTGCGACCCCAACTACTC 97

RESULT 14
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LOCUS      AF282635      139 bp      RNA      VRL      01-MAR-2001
DEFINITION Hepatitis C virus isolate H071 clone II 5' non-coding region
sequence.
ACCESSION  AF282635
VERSION     AF282635.1 GI:10764498
KEYWORDS
SOURCE      Hepatitis C virus.
ORGANISM    Hepatitis C virus.
REFERENCE   1 (bases 1 to 139)
AUTHORS     Harris,K.A. and Teo,C.G.
TITLE       Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
JOURNAL     Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED     11139197
REFERENCE   2 (bases 1 to 139)
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LOCUS AF282635 139 bp RNA VRL 01-MAR-2001
DEFINITION Hepatitis C virus isolate H075 clone I 5' non-coding region
sequence.
ACCESSION AF282635
VERSION AF282635.1 GI:10764498
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
Gradient Gel Electrophoresis
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 11139197
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK

FEATURES
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Best Local Similarity 95.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20
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Db 116 TTGCGACCCCAACTACTC 97

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LOCUS AF282637 139 bp RNA VRL 01-MAR-2001
DEFINITION Hepatitis C virus isolate H075 clone III 5' non-coding region
sequence.
ACCESSION AF282637
VERSION AF282637.1 GI:10764500
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
Gradient Gel Electrophoresis
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
PUBMED 11139197
REFERENCE 2 (bases 1 to 139)
AUTHORS Harris,K.A. and Teo,C.G.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
Central Public Health Laboratory, 61 Colindale Avenue, London NW9
5HT, UK

FEATURES
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/organism="Hepatitis C virus"
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Query Match 95.0%; Score 19; DB 14; Length 139;
Best Local Similarity 95.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20
|||
Db 116 TTGCGACCCCAACTACTC 97

Search completed: January 11, 2002, 06:41:09
Job time: 9725 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2002, 06:41:09 ; Search time 1759.97 Seconds
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Title: US-08-887-505-118
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Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_ba.*
- 2: gb_hig.*
- 3: gb_in.*
- 4: gb_lm.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
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- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
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- 25: em_sts.*
- 26: em_sy.*
- 27: em_un.*
- 28: em_vl.*
- 29: em_htgo_hum.*
- 30: em_htgo_inv.*
- 31: em_htgo_rnd.*
- 32: em_htgo_rnd.*
- 33: em_htg_hum.*
- 34: em_htg_inv.*
- 35: em_htg_rnd.*
- 36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Match	Length	DB	ID	Description
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2	18	90.0	27	6	ARI06359	ARI06359 Sequence
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5	18	90.0	33	6	AR097188	AR097188 Sequence
6	18	90.0	33	6	ARI30686	ARI30686 Sequence
7	18	90.0	33	6	I73295	I73295 Sequence 26
8	18	90.0	33	6	I82871	I82871 Sequence 50
9	18	90.0	40	6	ARI53179	ARI53179 Sequence
10	18	90.0	46	6	I44581	I44581 Sequence 10
11	18	90.0	46	6	I70986	I70986 Sequence 10
12	18	90.0	53	6	I44619	I44619 Sequence 48
13	18	90.0	53	6	I71024	I71024 Sequence 48
14	18	90.0	57	6	I73305	I73305 Sequence 36
15	18	90.0	64	6	I44601	I44601 Sequence 30
16	18	90.0	64	6	I71006	I71006 Sequence 30
17	18	90.0	138	14	HC081281	HC081281 Hepatitis C
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26	18	90.0	139	14	AF282639	AF282639 Hepatitis
27	18	90.0	139	14	AF282640	AF282640 Hepatitis
28	18	90.0	139	14	AF282641	AF282641 Hepatitis
29	18	90.0	139	14	AF282642	AF282642 Hepatitis
30	18	90.0	139	14	AF282643	AF282643 Hepatitis
31	18	90.0	139	14	AF282644	AF282644 Hepatitis
32	18	90.0	139	14	AF282645	AF282645 Hepatitis
33	18	90.0	139	14	AF282646	AF282646 Hepatitis
34	18	90.0	139	14	AY003921	AY003921 Hepatitis
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ALIGNMENTS

RESULT 1

I73297

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

I73297 23 bp DNA
Sequence 28 from patent US 5686272.

I73297
I73297.1 GI:3009436

Unknown.
Unclassified.

1 (bases 1 to 23)

Marshall, R.L., Carrino, J.J. and Sustachek, J.C.

Amplification of RNA sequences using the ligase chain reaction
Patent: US 5686272-A 28 11-NOV-1997;

Location/Qualifiers
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PAT 03-APR-1998

Query Match 90.0%; Score 18; DB 6; Length 23;
 Best Local Similarity 90.0%; Pred. No. 9.5;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCNACCCCAACACTACTC 20
 Db 2 TTTCGCAACCCCAACACTACTC 21

RESULT 2
 AR106359/c 27 bp DNA
 DEFINITION Sequence 21 from patent US 6107028.
 ACCESSION AR106359
 VERSION AR106359.1 GI:12820889
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Kay, M.A. and Lieber, A.
 TITLE Ribozymes for treating hepatitis C
 JOURNAL Patent: US 6107028-A 21 22-AUG-2000;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 BASE COUNT 6 a 4 c 12 g 5 t
 ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 27;
 Best Local Similarity 90.0%; Pred. No. 9.5;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCNACCCCAACACTACTC 20
 Db 24 TTTCGCGACCCCAACACTACTC 5

RESULT 3
 AR004396 33 bp DNA
 DEFINITION Sequence 50 from patent US 5747244.
 ACCESSION AR004396
 VERSION AR004396.1 GI:3965275
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Sheridan, P., Chang, C., Running, J., and Urdea, M.S.
 TITLE Nucleic acid probes immobilized on polystyrene surfaces
 JOURNAL Patent: US 5747244-A 50 05-MAY-1998;
 FEATURES Location/Qualifiers
 1..33
 /organism="unknown"
 BASE COUNT 8 a 13 c 6 g 6 t
 ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 33;
 Best Local Similarity 90.0%; Pred. No. 9.5;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCNACCCCAACACTACTC 20
 Db 10 TTTCGCGACCCCAACACTACTC 29

RESULT 4
 AR064935 33 bp DNA
 DEFINITION Sequence 126 from patent US 6190864.
 ACCESSION AR130686
 VERSION AR130686.1 GI:14119011
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J., and Urdea, M.S.
 TITLE HCV genomic sequences for diagnostics and therapeutics
 JOURNAL Patent: US 6190864-A 126 20-FEB-2001;
 FEATURES Location/Qualifiers

DEFINITION Sequence 60 from patent US 5849481.
 ACCESSION AR064935
 VERSION AR064935.1 GI:5995151
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Urdea, M.S., Horn, T., Chang, C., Warner, B., and Fultz, T.J.
 TITLE Nucleic acid hybridization assays employing large comb-type
 branched polynucleotides
 JOURNAL Patent: US 5849481-A 60 15-DEC-1998;
 FEATURES Location/Qualifiers
 1..33
 /organism="unknown"
 BASE COUNT 8 a 13 c 6 g 6 t
 ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 33;
 Best Local Similarity 90.0%; Pred. No. 9.5;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCNACCCCAACACTACTC 20
 Db 10 TTTCGCGACCCCAACACTACTC 29

RESULT 5
 AR097188 33 bp DNA
 DEFINITION Sequence 126 from patent US 6071693.
 ACCESSION AR097188
 VERSION AR097188.1 GI:12805918
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J., and Urdea, M.S.
 TITLE HCV genomic sequences for diagnostics and therapeutics
 JOURNAL Patent: US 6071693-A 126 06-JUN-2000;
 FEATURES Location/Qualifiers
 1..33
 /organism="unknown"
 BASE COUNT 8 a 13 c 6 g 6 t
 ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 33;
 Best Local Similarity 90.0%; Pred. No. 9.5;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCGCNACCCCAACACTACTC 20
 Db 10 TTTCGCGACCCCAACACTACTC 29

RESULT 6
 AR130686 33 bp DNA
 DEFINITION Sequence 126 from patent US 6190864.
 ACCESSION AR130686
 VERSION AR130686.1 GI:14119011
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Cha, T., Beall, E., Irvine, B., Kolberg, J., and Urdea, M.S.
 TITLE HCV genomic sequences for diagnostics and therapeutics
 JOURNAL Patent: US 6190864-A 126 20-FEB-2001;
 FEATURES Location/Qualifiers


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source
1..33
/organism="unknown"
BASE COUNT      8 a      13 c      6 g      6 t
ORIGIN

Query Match
Best Local Similarity 90.0%; Score 18; DB 6; Length 33;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
    ||||| ||||| |||||
Db 10 TTGCGACCCAACTACTC 29

RESULT 7
I73295/c
LOCUS
DEFINITION
Sequence 26 from patent US 5686272.
ACCESSION
I73295
VERSION
I73295.1 GI:3009434
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE
Amplification of RNA sequences using the ligase chain reaction
JOURNAL
Patent: US 5686272-A 26 11-NOV-1997;
FEATURES
Location/Qualifiers
1..33
source
/organism="unknown"
BASE COUNT.      5 a      4 c      14 g      10 t
ORIGIN

Query Match
Best Local Similarity 90.0%; Score 18; DB 6; Length 33;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
    ||||| ||||| |||||
Db 21 TTGCGACCCAACTACTC 2

RESULT 8
I82871
LOCUS
DEFINITION
Sequence 50 from patent US 5712383.
ACCESSION
I82871
VERSION
I82871.1 GI:3211168
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Sheridan,P., Chang,C., Running,J. and Urdea,M.S.
TITLE
Process for immobilizing nucleic acid probes on polystyrene
surfaces
JOURNAL
Patent: US 5712383-A 50 27-JAN-1998;
FEATURES
Location/Qualifiers
1..33
source
/organism="unknown"
BASE COUNT      8 a      13 c      6 g      6 t
ORIGIN

Query Match
Best Local Similarity 90.0%; Score 18; DB 6; Length 33;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
    ||||| ||||| |||||
Db 10 TTGCGACCCAACTACTC 29

RESULT 9
ARI53179/c
LOCUS
DEFINITION
Sequence 181 from patent US 6235480.
ACCESSION
ARI53179
VERSION
ARI53179.1 GI:15120711
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Shultz,J.William, Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,
Rhodes,R.Byron, Andrews,C.Ann, Hartnett,J.Robert, Gu,T.,
Olson,R.J., Wood,K.V. and Welch,R.
TITLE
Detection of nucleic acid hybrids
JOURNAL
Patent: US 6235480-A 181 22-MAY-2001;
FEATURES
Location/Qualifiers
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source
/organism="unknown"
BASE COUNT      6 a      8 c      16 g      10 t
ORIGIN

Query Match
Best Local Similarity 90.0%; Score 18; DB 6; Length 40;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
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Db 29 TTGCGACCCAACTACTC 10

RESULT 10
I44581
LOCUS
DEFINITION
Sequence 10 from patent US 5635352.
ACCESSION
I44581
VERSION
I44581.1 GI:2469294
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 46)
AUTHORS
Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE
Solution phase nucleic acid sandwich assays having reduced
background noise
JOURNAL
Patent: US 5635352-A 10 03-JUN-1997;
FEATURES
Location/Qualifiers
1..46
source
/organism="unknown"
BASE COUNT      9 a      17 c      11 g      9 t
ORIGIN

Query Match
Best Local Similarity 90.0%; Score 18; DB 6; Length 46;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCAACTACTC 20
    ||||| ||||| |||||
Db 10 TTGCGACCCAACTACTC 29

RESULT 11
I70986
LOCUS
DEFINITION
Sequence 10 from patent US 5681697.
ACCESSION
I70986
VERSION
I70986.1 GI:3007121
KEYWORDS

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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor
JOURNAL Patent: US 5681697-A 10 28-OCT-1997;
FEATURES Location/Qualifiers
 1. .46
 /organism="unknown"
BASE COUNT 9 a 17 c 11 g 9 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 46;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCCAACNCTACTC 20
 ||||| ||||||| |||||||
DB 10 TTGCGGACCCCAACTACTC 29

RESULT 12
LOCUS I44619 53 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 48 from patent US 5635352.
ACCESSION I44619
VERSION I44619.1 GI:2469332
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise
JOURNAL Patent: US 5635352-A 48 03-JUN-1997;
FEATURES Location/Qualifiers
 1. .53
 /organism="unknown"
BASE COUNT 13 a 18 c 11 g 11 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 53;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCCAACNCTACTC 20
 ||||| ||||||| |||||||
DB 30 TTGCGAACCCCAACTACTC 49

RESULT 13
LOCUS I71024 53 bp DNA PAT 03-APR-1998
DEFINITION Sequence 48 from patent US 5681697.
ACCESSION I71024
VERSION I71024.1 GI:3007159
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor
JOURNAL Patent: US 5681697-A 48 28-OCT-1997;
FEATURES Location/Qualifiers
 1. .53
 /organism="unknown"

BASE COUNT 13 a 18 c 11 g 11 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 53;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCCAACNCTACTC 20
 ||||| ||||||| |||||||
DB 30 TTGCGAACCCCAACTACTC 49

RESULT 14
LOCUS I73305/c 57 bp DNA PAT 03-APR-1998
DEFINITION Sequence 36 from patent US 5686272.
ACCESSION I73305
VERSION I73305.1 GI:3009444
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 57)
AUTHORS Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE Amplification of RNA sequences using the ligase chain reaction
JOURNAL Patent: US 5686272-A 36 11-NOV-1997;
FEATURES Location/Qualifiers
 1. .57
 /organism="unknown"
BASE COUNT 9 a 9 c 23 g 16 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 57;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCCAACNCTACTC 20
 ||||| ||||||| |||||||
DB 21 TTGCGAACCCCAACTACTC 2

RESULT 15
LOCUS I44601 64 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 30 from patent US 5635352.
ACCESSION I44601
VERSION I44601.1 GI:2469314
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 64)
AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
TITLE Solution phase nucleic acid sandwich assays having reduced background noise
JOURNAL Patent: US 5635352-A 30 03-JUN-1997;
FEATURES Location/Qualifiers
 1. .64
 /organism="unknown"
BASE COUNT 14 a 25 c 9 g 16 t
ORIGIN

Query Match 90.0%; Score 18; DB 6; Length 64;
Best Local Similarity 90.0%; Pred. No. 9.5;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGCGNACCCCAACNCTACTC 20
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DB 25 TTGCGAACCCCAACTACTC 44

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